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EXAMINER	
HUYNH, PHUONG N	

ART UNIT	PAPER NUMBER
1644	

DATE MAILED: 12/02/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/005,907	NOCKA ET AL.	
	Examiner	Art Unit	
	Phuong Huynh	1644	

-- The MAILING DATE of this communication app ars on the cover sheet with the correspondence address --

Period for R ply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *Three* MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *07 September 2004*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *72-87* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *72-73 and 78-87* is/are rejected.

7)☒ Claim(s) *74-77* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

1. Claims 72-87 are pending.

2. In view of the amendment filed 9/7/04, the following rejections remain.

3. Claims 72-73 and 78-87 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling only for (1) an isolated nucleic acid molecule encoding a protein differentially expressed in mast cell activated through the IgE receptor wherein the nucleic acid molecule encodes a polypeptide comprising SEQ ID NO: 2, (2) an isolated nucleic acid molecule encoding a protein differentially expressed in mast cell activated through the IgE receptor wherein the nucleic acid molecule comprises SEQ ID NO: 1, (3) an isolated nucleic acid molecule encoding a protein differentially expressed in mast cell activated through the IgE receptor wherein the nucleic acid molecule comprises nucleotides 25-432 of SEQ ID NO: 1, (4) an isolated nucleic acid molecule encoding a protein differentially expressed in mast cell activated through the IgE receptor wherein the nucleic acid molecule consists nucleotides 25-432 of SEQ ID NO: 1, (5) the isolated nucleic acid molecule mentioned above is operatively linked to one or more expression control elements, (6) an isolated host cell transformed with any one of said nucleic acid molecule, (7) A vector comprising nucleic acid molecule mentioned above, (8) a method of producing a polypeptide comprising culturing a host cell transformed with the nucleic acid mentioned above, and (9) a composition comprising any of the nucleic acid mentioned above, **does not** reasonably provide enablement for any isolated nucleic acid molecule as set forth in claims 72-73, and 78-87. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in **scope** with these claims.

Factors to be considered in determining whether undue experimentation is required to practice the claimed invention are summarized *In re Wands* (858 F2d 731, 737, 8 USPQ2d 1400, 1404 (Fed. Cir. 1988)). The factors most relevant to this rejection are the scope of the claim, the amount of direction or guidance provided, the lack of sufficient working examples, the unpredictability in the art and the amount of experimentation required to enable one of skill in the art to practice the claimed invention. The specification disclosure is insufficient

to enable one skilled in the art to practice the invention as broadly claimed without an undue amount of experimentation.

The specification discloses only an isolated nucleic acid molecule comprising SEQ ID NO: 1 that encodes the amino acid sequence of SEQ ID NO: 2, a vector and an isolated host cell comprising said nucleic acid molecule for producing said polypeptide. The specification further discloses that a change in the expression levels of said nucleic acid molecule is associated with allergic hypersensitivity in a patient. The specification discloses overexpression of polynucleotide reduces the release of degranulation as determined by marker β hexoseaminidase, decreases the release of PGD2, LTC4, and GM-CSF 18 hours after activation.

The specification does not teach how to make any nucleic acid molecule mentioned above because there is insufficient guidance as to the structure without the nucleotide sequence of any nucleic acid molecule "hybridizes under stringent conditions" (claims 72-73) to the complement of a nucleic acid encoding SEQ ID NO: 2 or the complement of a nucleic acid comprising SEQ ID NO: 1. There is insufficient guidance with respect to the length of the nucleic acid molecule without the nucleotide sequence that hybridizes to said complement or said nucleic acid molecule that encodes the amino acid sequence of SEQ ID NO: 2, and whether said nucleic acid molecule has the same function as SEQ ID NO: 1. Further, there is insufficient guidance about the specific hybridization condition used by applicant.

The state of the prior art as exemplified by Wallace *et al*, of record, is such that determining the specificity of hybridization probes is empirical by nature and the effect of mismatches within an oligonucleotide probe is unpredictable. Even if the probe is a 20mer, the total number of hits in a database search was 143,797,728, which suggest that some of the probes encompassed by the claims would not preferentially hybridize to the complement of SEQ ID NO: 1. Further, there is insufficient guidance as to the "hybridization conditions" used by applicant that is applicable to all undisclosed nucleic acid molecule. Given the unlimited number of undisclosed nucleic acid molecule, there is insufficient working example in the specification as filed. Since the nucleic acid molecule mentioned above is not enabled, it follows that any vector, host cell and composition comprising said nucleic acid molecule are not enabled.

With regard to nucleic acid molecule that encodes a protein that exhibits at least about 35% amino acid sequence identity to SEQ ID NO: 2 (claim 79), a "35% identity" means a 65% difference in the amino acid sequence alone. There is insufficient guidance as to which amino acids within the full length polypeptide of SEQ ID NO: 2, the corresponding polynucleotide, to

be substituted, deleted, or added and whether the resulting polypeptide encoded by the undisclosed nucleic acid molecule maintains its structure and function, not to mentioned the degeneracy of the genetic codon.

It is known in the art that the relationship between the amino acid sequence of a protein (polypeptide) and its tertiary structure (i.e. its binding activity) are not well understood and are not predictable (see Ngo et al., in The Protein Folding Problem and Tertiary Structure Prediction, 1994, Merz, et al., (ed.), Birkhauser, Boston, MA, pp. 433 and 492-495).

Skolnick *et al* teach that sequence-based methods for function prediction are inadequate and knowing a protein's structure does not tell one its function (See abstract, in particular).

Attwood *et al* teach that protein function is context-dependent and the state of the art of making functional assignments merely on the basis of some degree of similarity between sequences and the current structure prediction methods is unreliable (See figure, entire document).

Since the nucleic acid sequence of a polynucleotide determines its protein coding properties, predictability of which changes can be tolerated in a polynucleotide's nucleic acid sequence and still retain similar functions and properties requires a knowledge of, and guidance with regard to which nucleotide within the full-length nucleotide sequence, if any, are tolerant of modification and which are conserved or less tolerant to modification, and detailed knowledge of the ways in which the product's structure relates to its functional usefulness. Given the indefinite number of the additional nucleotides that may encompassed in the nucleic acid molecule of the instant claim 79, it is unpredictable which undisclosed polynucleotide will have the same structure and functions as the polynucleotide comprising SEQ ID NO: 1 that encodes SEQ ID NO: 2, in turn, would be useful for detecting allergic hypersensitivity in a patient.

Given the unlimited number of nucleic acid molecule, it is unpredictable which undisclosed nucleic acid molecule encodes a protein that has merely 35% sequence identity to SEQ ID NO: 2 would have the same function as SEQ ID NO: 2. Until the function of the polypeptide, the corresponding undisclosed nucleic acid molecule have been identified, it would take undue experimentation even for one skilled in the art to make and use the claimed nucleic acid molecule.

With regard to claim 78, the term "comprising" is open-ended. It expands the nucleotides 25-429 of SEQ ID NO: 1 to include additional nucleotides at either or both ends. There is a lack of guidance as to which nucleotides to be included and whether the resulting polynucleotide

maintains its structure and function as the nucleic acid molecule comprising SEQ ID NO: 1 or the open reading frame of comprises nucleotides 25-432 of SEQ ID NO: 1. Since the nucleic acid molecule mentioned above are not enabled, it follows that any vector, host cell method of making polypeptide using said nucleic acid molecule and composition comprising said nucleic acid molecule are not enabled.

For these reasons, it would require undue experimentation of one skilled in the art to practice the claimed invention. See page 1338, footnote 7 of Ex parte Aggarwal, 23 USPQ2d 1334 (PTO Bd. Pat App. & Inter. 1992). In re wands, 858 F.2d at 737, 8 USPQ2d at 1404 (Fed. Cir. 1988), the decision of the court indicates that the more unpredictable the area is, the more specific enablement is necessary. In view of the quantity of experimentation necessary, the limited working examples, the unpredictability of the art, the lack of sufficient guidance in the specification and the breadth of the claims, it would take an undue amount of experimentation for one skilled in the art to practice the claimed invention.

Applicants' arguments filed 9/7/04 have been fully considered but are not found persuasive.

Applicants' position is that the nature of the invention and state of the prior art on hybridization techniques stringent conditions were well known to the skilled artisan at the time the application was filed. Moreover, the specification adequately describes hybridization under stringent conditions in paragraph 0068 of the specification. The specification discloses SEQ ID NO: 2 and the nucleic acid encoding SEQ ID NO: 2. In the Examples, specifically Examples 1, 2, and 5, the specification discloses isolation and cloning of the MCI clone comprising SEQ ID NO: 2. Given this information and the state of the art, it does not require undue experimentation to obtain nucleic acids that hybridize under stringent conditions to the complement of the nucleic acid encoding SEQ ID NO; 2 and that encode a protein that is differentially expressed in activated mast cell. With regards to unpredictability of the invention, the Office Action states that changes in protein and nucleic acid sequences are unpredictable based on the cited references Ngo et al., Skolnick et al., Attwood et al. and Wallace et al. The cited references have been considered, but are not applicable to the present case because the claimed invention encompasses only those nucleic acid sequences that meet the limitations of the claims. The claims require that the nucleic acid molecules hybridize to the complement of SEQ ID NO: 2 under stringent conditions and encode a protein that is differentially expressed in activated mast cells. As discussed above, hybridization techniques under stringent conditions were well known at the time the application

was filed. The specification, specifically Examples 1, 2, and 5, provides guidance for isolating nucleic acids encoding proteins that are differentially expressed in an activated mast cell. Accordingly, the claimed invention is not unpredictable. Exparte Aggarwal and In re Wands have been considered. However, since the invention is not unreasonably claimed and not unpredictable as discussed above, the cited cases are not relevant. Regarding the number of working examples and amount of guidance, the specification provides sufficient guidance to enable one to practice the claimed invention. The specification, specifically Examples 1, 2, and 5, teaches how to isolate nucleic acids encoding proteins that are differentially expressed in activated mast cells. Paragraphs 00165 to 00176 and 00206 to 00209 of Examples 1, 2, and 5 describe MCI in detail. In paragraph 0068, the specification describes in detail hybridization under stringent conditions. Accordingly, the specification provides an adequate amount of guidance and working examples for practicing the claimed invention. It would not require undue experimentation to obtain the nucleic acids encompassed by the claims. Regarding the limitation of "35 % sequence identity" in claim 79, Applicants respectfully point out that the claims also require that the nucleic acid molecule hybridizes to the complement of a nucleic acid encoding SEQ ID NO: 2 under stringent conditions and encodes a protein differentially expressed in mast cells activated through the IgE receptor.

In contrast to applicants' assertion that hybridization techniques stringent conditions were well known to the skilled artisan at the time the application was filed, the state of the prior art as exemplified by Wallace *et al*, of record, is such that determining the specificity of hybridization probes is *empirical by nature* and the effect of mismatches within an oligonucleotide probe is unpredictable. Even if the probe is a 20mer, the total number of hits in a database search was 143,797,728, which suggest that some of the probes encompassed by the claims would not preferentially hybridize to the complement of SEQ ID NO: 1. Further, there is insufficient guidance as to the "hybridization conditions" used by applicant that is applicable to all undisclosed nucleic acid molecule. Given the unlimited number of undisclosed nucleic acid molecule, there is insufficient working example in the specification as filed. Since the nucleic acid molecule mentioned above is not enabled, it follows that any vector, host cell and composition comprising said nucleic acid molecule are not enabled. Further, the specific hybridizations used by applicants in the examples are not recited in the claims. Finally, nucleic acids encoding proteins that are differentially expressed in an activated mast cell does not equal to having a specific function.

With regard to nucleic acid molecule that encodes a protein that exhibits at least about 35% amino acid sequence identity to SEQ ID NO: 2 (claim 79), a "35% identity" means a 65% difference in the amino acid sequence alone. There is insufficient guidance as to which amino acids within the full length polypeptide of SEQ ID NO: 2, the corresponding polynucleotide, to be substituted, deleted, or added and whether the resulting polypeptide encoded by the undisclosed nucleic acid molecule maintains its structure and function, not to mentioned the degeneracy of the genetic codon.

It is known in the art that the relationship between the amino acid sequence of a protein (polypeptide) and its tertiary structure (i.e. its binding activity) are not well understood and are not predictable (see Ngo et al., in The Protein Folding Problem and Tertiary Structure Prediction, 1994, Merz, et al., (ed.), Birkhauser, Boston, MA, pp. 433 and 492-495).

Skolnick *et al* teach that sequence-based methods for function prediction are inadequate and knowing a protein's structure does not tell one its function (See abstract, in particular).

Attwood *et al* teach that protein function is context-dependent and the state of the art of making functional assignments merely on the basis of some degree of similarity between sequences and the current structure prediction methods is unreliable (See figure, entire document).

Since the nucleic acid sequence of a polynucleotide determines its protein coding properties, predictability of which changes can be tolerated in a polynucleotide's nucleic acid sequence and still retain similar functions and properties requires a knowledge of, and guidance with regard to which nucleotide within the full-length nucleotide sequence, if any, are tolerant of modification and which are conserved or less tolerant to modification, and detailed knowledge of the ways in which the product's structure relates to its functional usefulness. Given the indefinite number of the additional nucleotides that may encompassed in the nucleic acid molecule of the instant claim 79, it is unpredictable which undisclosed polynucleotide will have the same structure and functions as the polynucleotide comprising SEQ ID NO: 1 that encodes SEQ ID NO: 2, in turn, would be useful for detecting allergic hypersensitivity in a patient.

Given the unlimited number of nucleic acid molecule, it is unpredictable which undisclosed nucleic acid molecule encodes a protein that has merely 35% sequence identity to SEQ ID NO: 2 would have the same function as SEQ ID NO: 2. Until the function of the polypeptide, the corresponding undisclosed nucleic acid molecule have been identified, it would

take undue experimentation even for one skilled in the art to make and use the claimed nucleic acid molecule.

With regard to claim 78, the term "comprising" is open-ended. It expands the nucleotides 25-429 of SEQ ID NO: 1 to include additional nucleotides at either or both ends. There is a lack of guidance as to which nucleotides to be included and whether the resulting polynucleotide maintains its structure and function as the nucleic acid molecule comprising SEQ ID NO: 1 or the open reading frame of comprises nucleotides 25-432 of SEQ ID NO: 1. Since the nucleic acid molecule mentioned above are not enabled, it follows that any vector, host cell method of making polypeptide using said nucleic acid molecule and composition comprising said nucleic acid molecule are not enabled.

For these reasons, it would require undue experimentation of one skilled in the art to practice the claimed invention. See page 1338, footnote 7 of Ex parte Aggarwal, 23 USPQ2d 1334 (PTO Bd. Pat App. & Inter. 1992). In re wands, 858 F.2d at 737, 8 USPQ2d at 1404 (Fed. Cir. 1988), the decision of the court indicates that the more unpredictable the area is, the more specific enablement is necessary. In view of the quantity of experimentation necessary, the limited working examples, the unpredictability of the art, the lack of sufficient guidance in the specification and the breadth of the claims, it would take an undue amount of experimentation for one skilled in the art to practice the claimed invention.

4. Claims 72-73 and 78-87 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor, at the time the application was filed, had possession of the claimed invention.

The specification discloses only an isolated nucleic acid molecule comprising SEQ ID NO: 1 that encodes the amino acid sequence of SEQ ID NO: 2, a vector and an isolated host cell comprising said nucleic acid molecule for producing said polypeptide. The specification further discloses that a change in the expression levels of said nucleic acid molecule is associated with allergic hypersensitivity in a patient. The specification discloses overexpression of polynucleotide reduces the release of degranulation as determined by marker β hexoseaminidase, decreases the release of PGD2, LTC4, and GM-CSF 18 hours after activation.

The specification discloses only an isolated nucleic acid molecule comprising SEQ ID NO: 1 that encodes the amino acid sequence of SEQ ID NO: 2, a vector and an isolated host cell

comprising said nucleic acid molecule for producing said polypeptide. The specification further discloses that a change in the expression levels of said nucleic acid molecule is associated with allergic hypersensitivity in a patient. The specification discloses overexpression of polynucleotide reduces the release of degranulation as determined by marker β hexoseaminidase, decreases the release of PGD2, LTC4, and GM-CSF 18 hours after mast cell activation.

With the exception of the specific nucleic acid molecule comprising SEQ ID NO: 1 for detection of allergic hypersensitivity in a patient, there is inadequate written description about the structure associated with function of all nucleic acid molecule that hybridizes under stringent conditions to the complement of a nucleic acid encoding SEQ ID NO: 2 without the nucleotide sequence and the specific stringent conditions under which it hybridizes. Further, the hybridization conditions used by applicant are not recited in the claim. Likewise, there is inadequate written description about the nucleic acid molecules that hybridizes to the complement of a nucleic acid comprising SEQ ID NO: 1 without the nucleic acid sequence.

With regard to nucleic acid molecule that encodes a protein that exhibits at least about 35% amino acid sequence identity to SEQ ID NO: 2 (claim 1), a protein that exhibits "35% identity" means a 75% difference just the amino acid sequence alone, much less about the nucleic acid sequence. There is inadequate written about which amino acids within the full length polypeptide of SEQ ID NO: 2, the corresponding polynucleotide to be substituted, deleted, or added and whether the resulting polypeptide maintains the same structure and function as SEQ ID NO: 2. Without the nucleic acid sequence, applicant simply asks one of skilled in the art to go figure themselves what the claimed nucleic acid sequence look like. Since the nucleic acid sequence is not adequately described, it follows that the vector comprising said undisclosed nucleic acid sequence is not adequately described. It also follows that the host cell transformed with said undisclosed nucleic acid sequence is not adequately described. Likewise, a composition comprising said undisclosed nucleic acid sequence is not adequately described.

Given the lack of an additional nucleic acid molecule such as nucleic acid molecule that encodes a protein that exhibits at least about 35% amino acid sequence identity to SEQ ID NO: 2 as encompassed by the claims, one of skill in the art would reasonably conclude that the disclosure fails to provide a representative number of species to describe the genus. Thus, Applicant was not in possession of the claimed genus. *See University of California v. Eli Lilly and Co. 43 USPQ2d 1398; University of Rochester v. G.D. Searle & Co., 69 USPQ2d 1886 (CA FC2004).*

Applicant is directed to the Final Guidelines for the Examination of Patent Applications Under the 35 U.S.C. 112, ¶ 1 "Written Description" Requirement, Federal Register, Vol. 66, No. 4, pages 1099-1111, Friday January 5, 2001.

Applicants' arguments filed 9/7/04 have been fully considered but are not found persuasive.

Applicants' position is that the specification adequately describes the nucleic acid molecules encompassed by claim 72 and the dependent claims. As an example, paragraphs 00165-00176 and 00206-00209 describe the claimed invention in detail. Paragraph 0065 provides examples of the nucleic acids of the present invention, and paragraphs 00165-00176 provide guidance for the isolation of the nucleic acids of the present invention. Moreover, paragraph 0068 describes hybridization under high stringency conditions. Accordingly, the specification provides a description of the required structure of the claimed nucleic acids. Applicants also point the Examiner to the recent decision from the Board of Patent

Appeals and Interferences, Appeal No. 2002-2046 (see attached). The decision clearly states that the structure of a claim using the phrase "comprising" in the context of a disclosed sequence does not amount to a lack of written description for failure to describe "additional nucleic acids at either or both ends" as stated by the Examiner on page 4 of the Office Action. (See pages 25 and 26 of the decision.)

However, the specific hybridization conditions are not recited in the claims. Further, there is inadequate written description about the structure associated with function of all nucleic acid molecule that hybridizes under stringent conditions to the complement of a nucleic acid encoding SEQ ID NO: 2 without the nucleotide sequence. With regard to nucleic acid molecule that encodes a protein that exhibits at least about 35% amino acid sequence identity to SEQ ID NO: 2 (claim 1), a protein that exhibits "35% identity" means a 75% difference just the amino acid sequence alone, much less about the nucleic acid sequence. There is inadequate written about which amino acids within the full length polypeptide of SEQ ID NO: 2, the corresponding polynucleotide to be substituted, deleted, or added and whether the resulting polypeptide maintains the same structure and function as SEQ ID NO: 2. Without the nucleic acid sequence, applicant simply asks one of skilled in the art to go figure themselves what the claimed nucleic acid sequence look like. Since the nucleic acid sequence is not adequately described, it follows that the vector comprising said undisclosed nucleic acid sequence is not adequately described. It also follows that the host cell transformed with said undisclosed nucleic acid sequence is not

adequately described. Likewise, a composition comprising said undisclosed nucleic acid sequence is not adequately described. With regard to the Board of Patent Appeals and Interferences, Appeal No. 2002-2046, it is well settled that whether similar claims have been allowed to others is immaterial. See In re Giolito, 530 F.2d 397, 188 USPQ 645, 1976. Every case is examined on its own merits. The term "comprising" in claim 78 is open-ended. It expands the nucleic acid molecule comprises nucleotides 25-429 of SEQ ID NO: 1 to include additional nucleotide at either or both ends. There is inadequate written description as to which nucleotides at either or both ends to be included, much less about the function of the claimed nucleic acid molecule.

5. The rejections of claim 1 under 35 U.S.C. 102(a) as being anticipated by Waterston et al (Accession No AC 074365, Sept 2000, PTO 892) and claims 3 and 5 under 35 U.S.C. 102(a) as being anticipated by Accession No BF242113 (Strusberg, Nov 14, 2000) are hereby withdrawn in view of the amendment to the claim and the declaration by Karl Nocka, Gregorio Pirozzi, and Richard Einstein under 37 C.F.R. § 1.131 that the subject matter of pending claims 1-5, 23-29, and 49 was invented and reduced to practice before the-publication of the cited references.

6. The following new ground of rejection is necessitated by the amendment filed 9/7/04.

7. The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter, which the applicant regards as his invention.

8. Claims 83-84 and 86 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The term "A host cell" in claim 83 is indefinite and ambiguous because said host cell reads on host cell in an animal. It is suggested that the claim be amended to recite "An isolated host cell".

The "said host" in claim 84 has no antecedent basis in base claim 83 because claim 83 recites "A host cell", not "host". Further, the pleural "host cells" in claim 84 does not correlate with the singular "host cell".

The pleural "host cells" in claim 86, line 2 does not correlate with the singular "host cell" in claim 86 line 1.

9. Claims 74-77 are objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims.

10. No claim is allowed.

11. Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, THIS ACTION IS MADE FINAL. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

12. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Phuong Huynh "NEON" whose telephone number is (571) 272-0846. The examiner can normally be reached Monday through Friday from 9:00 am to 5:30 p.m. A message may be left on the examiner's voice mail service. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Christina Chan can be reached on (571) 272-0841. The IFW official Fax number is (703) 872-9306.

13. Any information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR

system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Phuong N. Huynh, Ph.D.
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November 23, 2004

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